

SEQUENCE LISTING

<110> CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS  
<110> BIONOSTRA, S.L.

<120> EMPTY CAPSIDS (VLPs (-VP4)) OF THE INFECTIOUS BURSAL DISEASE VIRUS  
(IBDV), OBTAINMENT PROCESS AND APPLICATIONS

<130> P1392PC

<150> ES P200400121  
<151> 2004-01-21 (January 21, 2004)

<160> 10  
<170> PatentIn version 3.1

<210> 1  
<211> 35  
<212> DNA  
<213> Artificial sequence

<220> Synthetic DNA  
<223> Oligo I primer

<400> 1  
gcgcagatct atgacaaacc tgtcagatca aaccc 35

<210> 2  
<211> 34  
<212> DNA  
<213> Artificial sequence

<220> Synthetic DNA  
<223> Oligo II primer

<400> 2  
gcgcaagctt aggcgagagt cagctgcctt atgc 34

<210> 3  
<211> 7595  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Plasmid pFBD/pVP2-his-VP3

<221> promoter  
<222> (157)..(285)  
<223> Promotor ppolh

<221> CDS  
<222> (291)..(1289)  
<223> pVP2 ORF



agg ctt ggt gac ccc att ccc gca ata ggg ctt gac cca aaa atg gta 872  
 Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys Met Val  
 180 185 190

gcc aca tgt gac agc agt gac agg ccc aga gtc tac acc ata act gca 920  
 Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile Thr Ala  
 195 200 205 210

gcc gat gat tac caa ttc tca tca cag tac caa cca ggt ggg gta aca 968  
 Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly Val Thr  
 215 220 225

atc aca ctg ttc tca gcc aac att gat gcc atc aca agc ctc agc gtt 1016  
 Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser Val  
 230 235 240

ggg gga gag ctc gtg ttt cga aca agc gtc cac ggc ctt gta ctg ggc 1064  
 Gly Gly Glu Leu Val Phe Arg Thr Ser Val His Gly Leu Val Leu Gly  
 245 250 255

gcc acc atc tac ctc ata ggc ttt gat ggg aca acg gta atc acc agg 1112  
 Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile Thr Arg  
 260 265 270

gct gtg gcc gca aac aat ggg ctg acg acc ggc acc gac aac ctt atg 1160  
 Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu Met  
 275 280 285 290

cca ttc aat ctt gtg att cca aca aac gag ata acc cag cca atc aca 1208  
 Pro Phe Asn Leu Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile Thr  
 295 300 305

tcc atc aaa ctg gag ata gtg acc tcc aaa agt ggt ggt cag gca ggg 1256  
 Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala Gly  
 310 315 320

gat cag atg tca tgg tgg gca aga ggg agc cta gcagtgcga tccatggtgg 1309  
 Asp Gln Met Ser Trp Ser Ala Arg Gly Ser Leu  
 325 330

caactatcca ggggccctcc gtcccgtcac gctagtggcc tacgaaagag tggcaacagg 1369

atccgtcggtt acggtcgctg ggggtgagcaa cttcgagctg atcccaaata ctgaactagc 1429

aaagaacctg gttacagaat acggccgatt tgacccagga gccatgaact acacaaaatt 1489

gatactgagt gagagggacc gtcttggtcat caagaccgtc tggccaacaa gggagtacac 1549

tgactttcgt gaatacttca tggaggtggc cgacctcaac totcccctga agattgcagg 1609

agcattcggc ttcaaagaca taatccgggc cataaggagg atagctgtgc cgggtggtctc 1669

cacattgttc ccacctgcg ctcacctagc ccatgcaatt ggggaagggtg tagactacct 1729

gctgggcgat gaggcccagg ccgcttcagg aactgctcga gccgcgtcag gaaaagcaag 1789

agctgcctca ggccgcataa ggcagctgac tctgcctaa gcttgctcag aagtactaga 1849

ggatcataat cagccatacc acattttagt aggttttact tgcttttaaaa aacctcccac 1909

acctccccct gaacctgaaa cataaaatga atgcaattgt tgttggttaac ttgtttattg 1969  
cagcttataa tgggttacaaa taaagcaata gcatcacaaa ttccacaaat aaagcatttt 2029  
tttcactgca ttctagtgtg ggtttgtcca aactcatcaa tgtatcttat catgtctgga 2089  
tctgatcact gcttgagcct aggagatccg aaccagataa gtgaaatcta gttccaaact 2149  
attttgtcat ttttaatttt cgtattagct tacgacgcta caccagttc ccatctattt 2209  
tgtcactctt ccctaaataa tccttaaaaa ctccatttcc acccctcca gttcccaact 2269  
attttgtccg cccacagcgg ggcatttttc ttctgttat gtttttaatc aaacatcctg 2329  
ccaactccat gtgacaaacc gtcactctog gctacttttt ctctgtcaca gaatgaaaat 2389  
ttttctgtca tctcttcgtt attaatgttt gtaattgact gaatatcaac gcttatttgc 2449  
agcctgaatg gcgaatggga cgcgccctgt agcggcgcat taagcgcggc ggggtgtggg 2509  
gttacgcgca gcgtgaccgc tacacttgcc agcgccctag cggccgctcc ttctgctttc 2569  
ttcccttctt ttctcgccac gttcgccggc ttccccgtc aagctctaaa tcgggggctc 2629  
cctttagggg tccgatttag tgctttacgg cacctcgacc ccaaaaaact tgattagggg 2689  
gatgggtcac gtagtgggcc atcgccctga tagacggttt ttcgcccttt gacgttgagg 2749  
tccacgttct ttaatagtgg actctgttc caaactggaa caaactcaa ccctatctcg 2809  
gtctattctt ttgatttata agggattttg ccgatttcgg cctattgggt aaaaaatgag 2869  
ctgatttaac aaaaatttaa cgcgaatttt aacaaaatat taacgtttac aatttcaggt 2929  
ggcacttttc ggggaaatgt gcgcggaacc cctatttgtt tatttttcta aatacattca 2989  
aatatgtatc cgctcatgag acaataaacc tgataaatgc ttcaataata ttgaaaaagg 3049  
aagagtatga gtattcaaca ttccgtgtc gcccttatc ctttttttgc ggcattttgc 3109  
cttcctgttt ttgctcacc agaaacgctg gtgaaagtaa aagatgctga agatcagttg 3169  
gggtgcacgag tgggttacat cgaactggat ctcaacagcg gtaagatcct tgagagtttt 3229  
cgccccgaag aacgttttcc aatgatgagc acttttaaaag ttctgctatg tggcgcggtg 3289  
ttatcccgtg ttgacgcgg gcaagagcaa ctcggtcgcc gcatacacta ttctcagaat 3349  
gacttggttg agtactcacc agtcacagaa aagcatctta cggatggcat gacagtaaga 3409  
gaattatgca gtgctgccat aaccatgagt gataaactg cggccaactt acttctgaca 3469  
acgatoggag gaccgaagga gctaaccgct tttttgcaca acatggggga tcatgtaact 3529  
cgccttgatc gttgggaacc ggagctgaat gaagccatac caaacgacga gcgtgacacc 3589  
acgatgcctg tagcaatggc aacaacgttg cgcaactat taactggcga actaacttact 3649  
ctagcttccc ggcaacaatt aatagactgg atggaggcgg ataaagtgtc aggaccactt 3709

ctgcgctcgg cccttcoggc tggctgggtt attgctgata aatctggagc cggtgagcgt 3769  
gggtctcgcg gtatcattgc agcactgggg ccagatggta agccctcccg tatcgtagtt 3829  
atctacacga cggggagtcg ggcaactatg gatgaacgaa atagacagat cgctgagata 3889  
ggtgccctcac tgattaagca ttggttaactg tcagaccaag tttactcata tatacttttag 3949  
attgatttaa aacttcattt ttaatttaaa aggatctagg tgaagatcct ttttgataat 4009  
ctcatgacca aaatccctta acgtgagttt tcgttccact gagcgtcaga ccccgtagaa 4069  
aagatcaaag gatcttcttg agatcccttt tttctgcgcg taatctgctg cttgcaaaca 4129  
aaaaaaccac cgctaccagc ggtggtttgt ttgccggatc aagagctacc aactcttttt 4189  
ccgaaggtaa ctggcttcag cagagcgcag ataccaaata ctgtccttct agtgtagccg 4249  
tagttaggcc accacttcaa gaactctgta gcaccgccta catacctcgc tctgctaata 4309  
ctgttaccag tggctgctgc cagtggcgat aagtcgtgtc ttaccgggtt ggactcaaga 4369  
cgatagttag cggtataagg gcagcggctg ggctgaacgg ggggttcgtg cacacagccc 4429  
agcttggagc gaacgacctc caccgaactg agatacctac agcgtgagca ttgagaaagc 4489  
gccacgcttc ccgaaggagc aaaggcggac aggtatccgg taagcggcag ggtcggaaca 4549  
ggagagcgca cgagggagct tccaggggga aacgcctggc atctttatag tccgtgctggg 4609  
tttcgccacc tctgacttga gcgtcgattt ttgtgatgct cgtcaggggg gcggagccta 4669  
tggaaaaacg ccagcaacgc ggccttttta cggttcctgg ccttttgctg gccttttgct 4729  
cacatgttct ttcctgcgtt atcccctgat tctgtggata accgtattac cgcctttgag 4789  
tgagctgata ccgctcgccg cagccgaacg accgagcgca gcgagtcagt gagcgaggaa 4849  
gcggaagagc gcctgatgcg gtattttctc cttacgcata tgtgcggtat ttcacaccgc 4909  
agaccagccg cgtaacctgg caaatcggt tacggttgag taataaatgg atgccctgcg 4969  
taagcgggtg tggcgggaca ataaagtctt aaactgaaca aaatagatct aaactatgac 5029  
aataaagtct taaactagac agaatagttg taaactgaaa tcagtccagt tatgctgtga 5089  
aaaagcatatc tggacttttg ttatggctaa agcaaactct tcattttctg aagtgcaaata 5149  
tgcccgtcgt attaaagagg ggcgtggcca agggcatggc aaagactata ttcgcggcgt 5209  
tgtgacaatt taccgaacaa ctccgcggcc ggggaagccga tctcggcttg aacgaattgt 5269  
taggtggcgg tacttggtgc gatatacaag tgcatactt cttcccgtat gcccaacttt 5329  
gtatagagag cactgcggg atcgtcacgc taatctgctt gcacgtagat cacataagca 5389  
ccaagcgcgt tggcctcatg cttgaggaga ttgatgagcg cgggtggcaat gccctgcctc 5449  
cgtgtctcgc cggagactgc gagatcatag atatagatct cactacgcgg ctgctcaaac 5509

ctgggcagaa cgtaagccgc gagagcgcca acaaccgctt cttggtcgaa ggcagcaagc 5569  
gcgatgaatg tcttactacg gagcaagtcc cggaggtaat cggagtcggg ctgatgttgg 5629  
gagtaggtgg ctacgtctcc gaactcacga ccgaaaagat caagagcagc ccgcatggat 5689  
ttgacttggg cagggccgag cctacatgtg cgaatgatgc ccatacttga gccacctaac 5749  
tttgtttttag ggcgactgcc ctgctgcgta acatcgttgc tgctgcgtaa catcgttgct 5809  
gctccataac atcaaacatc gaccacggc gtaacgcgct tgctgcttgg atgcccgagg 5869  
catagactgt acaaaaaaac agtcataaca agccatgaaa accgccactg cgccgttacc 5929  
accgctgcgt tcggtcaagg ttctggacca gttgcgtgag cgcatacgt acttgcat 5989  
cagtttacga accgaacagg cttatgtcaa ctgggttcgt gccttcaccc gtttccacgg 6049  
tgtgcgtcac ccggcaacct tgggcagcag cgaagtcgag gcatttctgt cctggctggc 6109  
gaacgagcgc aaggtttcgg tctccacgca tcgtcaggca ttggcggcct tgctgttctt 6169  
ctacggcaag gtgctgtgca cggatctgcc ctggcttcag gagatcggta gacctcggcc 6229  
gtcgcggcgc ttgccggtgg tgctgacccc ggatgaagtg gttcgcaccc tcggttttct 6289  
ggaaggcgag catcgtttgt tcgccagga ctctagctat agttctagt gttggcctac 6349  
gtacccgtag tggctatggc agggcttgcc gccccgacgt tggctgcgag ccctgggcct 6409  
tcaccggaac ttgggggttg ggggtgggaa aaggaagaaa cgcgggcgta ttggtcccaa 6469  
tggggctctg gtgggtatc gacagagtgc cagccctggg accgaacccc gcgtttatga 6529  
acaaacgacc caacaccggt gcgttttatt ctgtcttttt attgccgtca tagcgcgggt 6589  
tccttccggt attgtctcct tccgtgttcc agttagctc ccccatctcc cggtagcgca 6649  
tgctcagaga ctgcaggctc tagattcgaa agcggccgcg actagtgagc tcgtcgacgt 6709  
aggcctttga attccggatc ctactcaag gtctcatca gagacggtcc tgatccagcg 6769  
gccagccga ccagggggtc tctgtgttgg agcattgggt tttggcttgg gctttggtag 6829  
agccgcctg ggattgcgat gcttcatctc catcgacgtc aagagcagat ctttcatctg 6889  
ttcttggttt gggccacgtc catggttgat ttcatagact ttggcaactt cgtctatgaa 6949  
agcttggggg ggtcttgct gtcttgagc cccgtagatc gacgtagctg cccttaggat 7009  
ttgttcttct gatgccaacc ggctcttctc tgcatgcacg tagtctagat agtctcgtt 7069  
tgggtccggt atttctcgtt tgttctgcca gtactttacc tggcctgggc ttggccctcg 7129  
gtgcccattg agtgctaccc attctggtgt tgcaaagtag atgcccatgg totocatctt 7189  
ctttgagatc cgtgtgtctt tttccctctg tgcttctct ggtgtggggc cccgagcctc 7249  
cactccgtag cctgctgtcc cgtacttggc cctttgcgac ttgctgcctg cttgtggtgc 7309

gtttgcaaga aaatttcgca tccgatgggc gttcgggtcg ctgagtgcga agttggccat 7369  
 gtcagtcaca atcccattct cttccagcca catgaacaca ctgagtgcag attggaatag 7429  
 tgggtccacg ttggtgctg cttccattgc tctgacggca ctctcgagtt cgggggtctc 7489  
 tttgaactct gatgcagcca tggcgccctg aaaatacagg ttttcggtcg ttgggatatc 7549  
 gtaatcgtga tgggtgatggg gatggtagta cgacatgggt tcggac 7595

<210> 4  
 <211> 333  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> pVP2-his-VP3 protein

<400> 4  
 Met Thr Asn Leu Ser Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg  
 1 5 10 15  
 Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr  
 20 25 30  
 Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr  
 35 40 45  
 Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro  
 50 55 60  
 Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Gly Asn Gly Asn Tyr  
 65 70 75 80  
 Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr  
 85 90 95  
 Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr  
 100 105 110  
 Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr  
 115 120 125  
 Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu  
 130 135 140  
 Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val  
 145 150 155 160  
 Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly  
 165 170 175  
 Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys  
 180 185 190  
 Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile  
 195 200 205

Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly  
 210 215 220  
 Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu  
 225 230 235 240  
 Ser Val Gly Gly Glu Leu Val Phe Arg Thr Ser Val His Gly Leu Val  
 245 250 255  
 Leu Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile  
 260 265 270  
 Thr Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn  
 275 280 285  
 Leu Met Pro Phe Asn Leu Val Ile Pro Thr Asn Glu Ile Thr Gln Pro  
 290 295 300  
 Ile Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln  
 305 310 315 320  
 Ala Gly Asp Gln Met Ser Trp Ser Ala Arg Gly Ser Leu  
 325 330

<210> 5  
 <211> 35  
 <212> DNA  
 <213> Artificial sequence

<220> Synthetic DNA  
 <223> Oligo III primer

<400> 5  
 gcgcagatct atgacaaacc tgtcagatca aaccc

35

<210> 6  
 <211> 34  
 <212> DNA  
 <213> Artificial sequence

<220> Synthetic DNA  
 <223> Oligo IV primer

<400> 6  
 gcgcaagctt aggcgagagt cagctgcctt atgc

34

<210> 7  
 <211> 33  
 <212> DNA  
 <213> Artificial sequence

<220> Synthetic DNA  
 <223> Oligo V primer

<400> 7  
 gcgcgaattc gatggcatca gagttcaaag aga

33



<210> 8  
 <211> 32  
 <212> DNA  
 <213> Artificial sequence

<220> Synthetic DNA  
 <223> Oligo VI primer

<400> 8  
 cgcgatccc tcaaggtcct catcagagac gg

32

<210> 9  
 <211> 9600  
 <212> DNA  
 <213> Artificial sequence

<223> Plasmid pESCURA/pVP2-VP3-GFP

<221> promoter  
 <222> (5649)..(5859)  
 <223> Promoter GAL 1 (pVP2)

<221> promoter  
 <222> (7402)..(8080)  
 <223> Promoter GAL 2 (VP3-GFP)

<221> CDS  
 <222> (8086)..(9597)  
 <223> VP3-GFP ORF

<400> 9  
 ggccgcacta gtatcgatgg attacaagga tgacgacgat aagatctgag ctottaatta 60  
 acaattcttc gccagagggt tggtaagtc tccaatcaag gttgtcggct tgtctacctt 120  
 gccagaaatt tacgaaaaga tggaaaaggg tcaaatcggt ggtagatacg ttgttgacac 180  
 ttctaaataa gcgaatttct tatgatttat gatttttatt attaaataag ttataaaaaa 240  
 aataagtgtg tacaaatttt aaagtgactc ttaggtttta aaacgaaaat tcttattctt 300  
 gagtaactct ttctgttagg tcaggttget ttctcaggta tagcatgagg tcgctccaat 360  
 tcagctgcat taatgaatcg gccaacgcgc ggggagaggc gggttgcgta ttgggcgctc 420  
 ttccgcttcc tcgctcactg actcgctgcg ctcggctcgtt cggctgcggc gagcggtatc 480  
 agctcactca aaggcggtaa tacggttatc cacagaatca ggggataacg caggaaagaa 540  
 catgtgagca aaaggccagc aaaaggccag gaaccgtaaa aaggccgcgt tgctggcggt 600  
 ttccataggt ctcgcccccc ctgacgagca tcacaaaaat cgacgctcaa gtcagagggtg 660  
 gcgaaacccg acaggactat aaagatacca ggcgtttccc cctggaagct ccctogtgcg 720  
 ctctcctgtt ccgaccctgc cgcttaccgg atacctgtcc gcctttctcc cttcgggaag 780  
 cgtggcgctt tctcatagct cacgctgtag gtatctcagt tcggtgtagg tcgttcgctc 840

caagctgggc tgtgtgcacg aacccccgt tcagcccgac cgtgcgct tatccggtaa 900  
ctatcgtctt gagtccaacc cggtaagaca cgacttatcg ccactggcag cagccactgg 960  
taacaggatt agcagagcga ggtatgtagg cggtgctaca gagttcttga agtggtggcc 1020  
taactacggc tacactagaa ggacagtatt tggatatctgc gctctgctga agccagttac 1080  
cttcggaaaa agagttggta gctcttgatc cggcaaaaa accaccgctg gtagcggtagg 1140  
tttttttggt tgcaagcagc agattacgcg cagaaaaaa ggatctcaag aagatccttt 1200  
gatcttttct acggggctctg acgctcagtg gaacgaaaac tcacgttaag ggattttggt 1260  
catgagatta tcaaaaagga tottcaccta gatcctttta aattaaaaat gaagttttaa 1320  
atcaatctaa agtatatatg agtaaaacttg gtctgacagt taccaatgct taatcagtga 1380  
ggcacctatc tcagcgatct gtctatctcg ttcattcata gttgcctgac tccccgtcgt 1440  
gtagataact acgatacggg agggcttacc atctggcccc agtgctgcaa tgataccgcg 1500  
agaccacgc tcaccggctc cagatttatc agcaataaac cagccagccg gaagggccga 1560  
gcgcagaagt ggtcctgcaa ctttatccgc ctccatccag tctattaatt gttgccggga 1620  
agctagagta agtagttcgc cagttaatag tttgcgcaac gttgttgcca ttgctacagg 1680  
catcgtggtg tcacgctcgt cgtttggtat ggcttcattc agctccggtt cccaacgatc 1740  
aaggcgagtt acatgatccc catgtttgag caaaaaagcg gttagctcct tcggtcctcc 1800  
gatcgttgct agaagtaagt tggccgcagt gttatcactc atggttatgg cagcaactgca 1860  
taattctctt actgtcatgc catccgtaag atgcttttct gtgactggtg agtactcaac 1920  
caagtcattc tgagaatagt gtatgcggcg accgagttgc tottgccgg cgtcaatacg 1980  
ggataatacc gcgccacata gcagaacttt aaaagtgtc atcattggaa aacgttcttc 2040  
ggggcgaaaa ctctcaagga tottaccgct gttgagatcc agttcgatgt aaccactcg 2100  
tgcaaccaac tgatcttcag catcttttac tttcaccagc gttcttggt gagcaaaaac 2160  
aggaaggcaa aatgccgcaa aaaagggaat aaggcgaca cggaaatgtt gaatactcat 2220  
actcttcctt tttcaatatt attgaagcat ttatcagggt tattgtctca tgagcggata 2280  
catatttgaa tgtatttaga aaaataaaca aataggggtt ccgcgcacat tccccgaaa 2340  
agtgccacct gaacgaagca tctgtgcttc atttttaga acaaaaatgc aacgcgagag 2400  
cgctaatttt tcaaacaag aatctgagct gcatttttac agaacagaaa tgcaacgcga 2460  
aagcgtatt ttaccaacga agaactctgtg ctcatTTTT gtaaaacaaa aatgcaacgc 2520  
gagagcgcta atttttcaaa caaagaatct gagctgcatt tttacagaac agaaatgcaa 2580  
cgcgagagcg ctattttacc acaagaat ctatacttct tttttgttct acaaaaatgc 2640

atcccgagag cgctatTTTT ctaacaaagc atcttagatt actTTTTTtc tcctttgtgc 2700  
gctctataat gcagttctctt gataactttt tgcaactgtag gtccgttaag gttagaagaa 2760  
ggctactttg gtgtctatTT tctcttccat aaaaaaagcc tgactccact tcccgcgttt 2820  
actgattact agcgaagctg cgggtgcatt ttttcaagat aaaggcatcc ccgattatat 2880  
tctataccga tgtggattgc gcatactttg tgaacagaaa gtgatagcgt tgatgattct 2940  
tcattgggtca gaaaattatg aacggtttct tctatTTTgt ctctatatac tacgtatagg 3000  
aaatgtttac attttctgtat tgttttcgat tcaactctatg aatagttctt actacaattt 3060  
ttttgtctaa agagtaatac tagagataaa cataaaaaat gtagaggctg agtttagatg 3120  
caagttcaag gagcgaaagg tggatgggta gggtatatag ggatatagca cagagatata 3180  
tagcaaagag atacttttga gcaatgtttg tggaagcggg attcgcaata ttttagtagc 3240  
tcgttacagt ccggtgcgtt tttggttttt tgaaagtgcg tcttcagagc gcttttggtt 3300  
ttcaaaagcg ctctgaagtt cctatacttt ctagagaata ggaacttcgg aataggaact 3360  
tcaaagcgtt tccgaaaacg agcgttccg aaaatgcaac gcgagctgcg cacatacagc 3420  
tcaactgttca cgtcgcacct atatctcgtt gttgcctgta tatatatata catgagaaga 3480  
acggcatagt gcgtgtttat gcttaaagtc gtacttatat gcgtctatTT atgtaggatg 3540  
aaaggtagtc tagtacctcc tgtgatatta tccattcca tcggggggtat cgtatgcttc 3600  
cttcagcact acccttttagc tgttctatat gctgccactc ctcaattgga ttagtctcat 3660  
ccttcaatgc tatcatttcc tttgatattg gatcatacta agaaaccatt attatcatga 3720  
cattaaccta taaaaatagg cgtatcacga ggccctttcg tctcgcgcgt ttoggtgatg 3780  
acggtgaaaa cctctgacac atgcagctcc cggagacggg cacagcttgt ctgtaagcgg 3840  
atgccgggag cagacaagcc cgtcagggcg cgtcagcggg tgttggcggg tgcggggct 3900  
ggcttaacta tgcggcatca gagcagattg tactgagagt gcaccatacc acagcttttc 3960  
aattcaattc atcattTTTT ttttattctt ttttttgatt tcggtttctt tgaaattttt 4020  
ttgattcggg aatctccgaa cagaaggaag aacgaaggaa ggagcacaga cttagattgg 4080  
tatatatagc catatgtagt gttgaagaaa catgaaattg ccagtatTC ttaaccaac 4140  
tgcacagAAC aaaaacctgc aggaacgaa gataaatcat gtcgaaagct acatataagg 4200  
aacgtgctgc tactcatcct agtcctgttg ctgccaagct atttaatatc atgcacgaaa 4260  
agcaaacaaa cttgtgtgct tcattggatg ttcgtaccac caaggaatta ctggagttag 4320  
ttgaagcatt aggtcccaaa atttgtttac taaaaacaca tgtggatatc ttgactgatt 4380  
tttccatgga gggcacagtt aagccgctaa aggcattatc cgccaagtac aattttttac 4440

tcttcgaaga cagaaaaattt gctgacattg gtaatacagt caaattgcag tactctgcgg 4500  
gtgtatacag aatagcagaa tgggcagaca ttacgaatgc acacggtgtg gtgggcccag 4560  
gtattgttag cggtttgaag caggcggcag aagaagtaac aaaggaacct agaggccttt 4620  
tgatgttagc agaattgtca tgcaagggtc ccctatctac tggagaatat actaagggtg 4680  
ctgttgacat tgcgaagagc gacaaagatt ttgttatcgg ctttattgct caaagagaca 4740  
tgggtggaag agatgaagggt tacgattggt tgattatgac acccggtgtg ggtttagatg 4800  
acaagggaga cgcattgggt caacagtata gaaccgtgga tgatgtggtc tctacaggat 4860  
ctgacattat tattgttgga agaggactat ttgcaaaggg aagggatgct aaggtagagg 4920  
gtgaacgtta cagaaaagca ggctgggaag catatttgag aagatgcggc cagcaaaact 4980  
aaaaaactgt attataagta aatgcatgta tactaaactc acaaattaga gcttcaattt 5040  
aattatatca gttattacc c tatgcggtgt gaaataccgc acagatgcgt aaggagaaaa 5100  
taccgcatac ggaaattgta aacgttaata ttttggttaa attcgcgtta aatttttgtt 5160  
aaatcagctc attttttaac caataggccg aaatcgcaa aatcccttat aaatcaaaag 5220  
aatagaccga gatagggttg agtggtgttc cagtttgtaa caagagtcca ctattaaaga 5280  
acgtggactc caacgtcaaa gggcgaaaaa cgcctatca gggcgatggc ccactacgtg 5340  
aaccatcacc ctaatcaagt tttttggggt cgaggtgccg taaagcacta aatcggaacc 5400  
ctaaaggag ccccgattt agagcttgac ggggaaagcc ggcgaaactg gcgagaaagg 5460  
aagggaagaa agcgaagga gcgggcgcta gggcgctggc aagtgtagcg gtcacgctgc 5520  
gcgtaaccac cacaccgcc gcgcttaatg cgccgctaca gggcgctcg cgccattcgc 5580  
cattcaggct gcgcaactgt tgggaagggc gatcggtgcg ggctcttcg ctattacgcc 5640  
agctggatct tcgagcgcc caaaacctt tcaagcaagg ttttcagtat aatgttacat 5700  
gcgtacacgc gtctgtacag aaaaaaaga aaaatttgaa atataaataa cgttcttaat 5760  
actaacataa ctataaaaaa ataaataggg acctagactt caggttgtct aactccttc 5820  
tttcgggtta gagcggatct tagctagccg cggtaccaag cttaggcgag agtcagctgc 5880  
cttatgcggc ctgaggcagc tcttgctttt cctgacgcgg ctcgagcagt tcctgaagcg 5940  
gcctgggct catcgcccag caggtagtct acaccttccc caattgcatg ggctagggga 6000  
gcggcagggtg ggaacaatgt ggagaccacc ggcacagcta tcctccttat ggcccgatt 6060  
atgtctttga agccgaatgc tcctgcaatc ttcaggggag agttgaggtc ggccaacctc 6120  
atgaagtatt cacgaaagtc agtgactcc cttgttgcc agacggtctt gatgccaaga 6180  
cggtccctct cactcagtat caattttgtg tagttcatgg ctctgggtc aaatcggccg 6240

tattctgtaa ccaggttctt tgctagtcca ggatttgga tcagctcgaa gttgctcacc 6300  
ccagcgaccg taacgacgga tcctgttgcc actctttcgt aggccactag cgtgacggga 6360  
cggagggccc ctggatagtt gccaccatgg atcgctactg ctaggctccc tcttgccgac 6420  
catgacatct gatccoctgc ctgaccacca cttttggagg tcactatctc cagtttgatg 6480  
gatgtgattg gctgggttat ctcgtttggt ggaatcaca gattgaatgg cataaggttg 6540  
tcggtgccgg tcgtcagccc attgtttgcg gccacagccc tgggtgattac cgttgtccca 6600  
tcaaagccta tgaggtagat ggtggcgccc agtacaaggc cgtggacgct tgttcgaaac 6660  
acgagctctc cccaacgct gaggcttggt atggcatcaa tgttggtga gaacagtgtg 6720  
attgttacct cacctggttg gtactgtgat gagaattggt aatcatcggc tgcagttatg 6780  
gtgtagactc tgggcctgtc actgctgtca catgtggcta ccatttttgg gtcaagccct 6840  
attgcgggaa tggggtcacc aagcctcaca tacccaagat catatgatgt gggtaagctg 6900  
aggacggtga ccccttcccc tactaggacg ttcccaattt tgtcgttgat gttggctgtt 6960  
gcagacatca acccattgta gctaacatct gtcagttcac tcaggcttcc ttggaaggtc 7020  
acggcgttta tggtgccgtt tagtgcataa acgccaccag gaagtgtgct tgacctcact 7080  
gtgagactcc gactcactag cctgcagtag ttgtaactgg ccggtaggtt ctgggcagtc 7140  
aggagcatct gatcgaactt gtagttccca ttgccctgca gtgtgtagtg agcaccacca 7200  
attgagccag ggaatccagg gaaaaagaca attagccctg accctgtgtc cccacagtc 7260  
aaattgtagg tcgaggtctc tgacctgaga gtgtgcttct ccagggtgtc gtccggaatg 7320  
gacgccggtc cggttggttg catcagaagg ctccgtatga acggaacaat ctgctgggtt 7380  
tgatctgaca ggtttgatcat agatccgggg tttttctctc ttgacgttaa agtatagagg 7440  
tatattaaca attttttggt gatactttta ttacatttga ataagaagta atacaaaccg 7500  
aaaatggtga aagtattagt taaagtgggt atgcagtttt tgcatttata tatctgttaa 7560  
tagatcaaaa atcatcgctt cgctgattaa ttacccacaga aataaggcta aaaaactaat 7620  
cgcattatca tcctatgggt gttaatttga ttcgttcatt tgaaggtttg tggggccagg 7680  
ttactgcaa tttttctctc tcataacat aaaagctagt attgtagaat ctttattgtt 7740  
cggagcagtg cggcgcgagg cacatctgcg tttcaggaac gcgaccggtg aagacgagga 7800  
cgcacggagg agagtcttcc ttcggagggc tgtcaccgc tcggcggtt ctaatccgta 7860  
cttcaatata gcaatgagca gttaagcgta ttactgaaag ttccaaagag aaggtttttt 7920  
taggctaaga taatggggct ctttacattt ccacaacata taagtaagat tagatatgga 7980  
tatgtatatg gatatgtata tggtggtaat gccatgtaat atgattatta aacttctttg 8040

cg	tc	ca	tc	ca	aaaaaaa	agt	aaga	attttt	gaaa	attcga	attcg	atg	gct	gca	tca	8097
													Met	Ala	Ala	Ser
												1				
gag	ttc	aaa	gag	acc	ccc	gaa	ctc	gag	agt	gcc	gtc	aga	gca	atg	gaa	8145
Glu	Phe	Lys	Glu	Thr	Pro	Glu	Leu	Glu	Ser	Ala	Val	Arg	Ala	Met	Glu	
5					10					15					20	
gca	gca	gcc	aac	gtg	gac	cca	cta	ttc	caa	tct	gca	ctc	agt	gtg	ttc	8193
Ala	Ala	Ala	Asn	Val	Asp	Pro	Leu	Phe	Gln	Ser	Ala	Leu	Ser	Val	Phe	
				25					30					35		
atg	tgg	ctg	gaa	gag	aat	ggg	att	gtg	act	gac	atg	gcc	aac	ttc	gca	8241
Met	Trp	Leu	Glu	Glu	Asn	Gly	Ile	Val	Thr	Asp	Met	Ala	Asn	Phe	Ala	
			40					45					50			
ctc	agc	gac	ccg	aac	gcc	cat	cgg	atg	cga	aat	ttt	ctt	gca	aac	gca	8289
Leu	Ser	Asp	Pro	Asn	Ala	His	Arg	Met	Arg	Asn	Phe	Leu	Ala	Asn	Ala	
			55				60					65				
cca	caa	gca	ggc	agc	aag	tcg	caa	agg	gcc	aag	tac	ggg	aca	gca	ggc	8337
Pro	Gln	Ala	Gly	Ser	Lys	Ser	Gln	Arg	Ala	Lys	Tyr	Gly	Thr	Ala	Gly	
	70					75					80					
tac	gga	gtg	gag	gct	cgg	ggc	ccc	aca	cca	gag	gaa	gca	cag	agg	gaa	8385
Tyr	Gly	Val	Glu	Ala	Arg	Gly	Pro	Thr	Pro	Glu	Glu	Ala	Gln	Arg	Glu	
85					90					95					100	
aaa	gac	aca	cgg	atc	tca	aag	aag	atg	gag	acc	atg	ggc	atc	tac	ttt	8433
Lys	Asp	Thr	Arg	Ile	Ser	Lys	Lys	Met	Glu	Thr	Met	Gly	Ile	Tyr	Phe	
				105					110					115		
gca	aca	cca	gaa	tgg	gta	gca	ctc	aat	ggg	cac	cga	ggg	cca	agc	cca	8481
Ala	Thr	Pro	Glu	Trp	Val	Ala	Leu	Asn	Gly	His	Arg	Gly	Pro	Ser	Pro	
			120					125					130			
ggc	cag	gta	aag	tac	tgg	cag	aac	aaa	cga	gaa	ata	ccg	gac	cca	aac	8529
Gly	Gln	Val	Lys	Tyr	Trp	Gln	Asn	Lys	Arg	Glu	Ile	Pro	Asp	Pro	Asn	
		135					140					145				
gag	gac	tat	cta	gac	tac	gtg	cat	gca	gag	aag	agc	cgg	ttg	gca	tca	8577
Glu	Asp	Tyr	Leu	Asp	Tyr	Val	His	Ala	Glu	Lys	Ser	Arg	Leu	Ala	Ser	
	150					155					160					
gaa	gaa	caa	atc	cta	agg	gca	gct	acg	tcg	atc	tac	ggg	gct	cca	gga	8625
Glu	Glu	Gln	Ile	Leu	Arg	Ala	Ala	Thr	Ser	Ile	Tyr	Gly	Ala	Pro	Gly	
165					170					175					180	
cag	gca	gag	cca	ccc	caa	gct	ttc	ata	gac	gaa	gtt	gcc	aaa	gtc	tat	8673
Gln	Ala	Glu	Pro	Pro	Gln	Ala	Phe	Ile	Asp	Glu	Val	Ala	Lys	Val	Tyr	
				185					190					195		
gaa	atc	aac	cat	gga	cgt	ggc	cca	aac	caa	gaa	cag	atg	aaa	gat	ctg	

cca aag ccc aag cca aaa ccc aat gct cca aca cag aga ccc cct ggt Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr Gln Arg Pro Pro Gly 230 235 240	8817
cgg ctg ggc cgc tgg atc agg acc gtc tct gat gag gac ctt gag gga Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp Glu Asp Leu Glu Gly 245 250 255 260	8865
tcc atc gcc acc atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg Ser Ile Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val 265 270 275	8913
gtg ccc atc ctg gtc gag ctg gac ggc gac gta aac ggc cac aag ttc Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 280 285 290	8961
agc gtg tcc ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg acc Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 295 300 305	9009
ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 310 315 320	9057
ctc gtg acc acc ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 325 330 335 340	9105
gac cac atg aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 345 350 355	9153
tac gtc cag gag cgc acc atc ttc ttc aag gac gac ggc aac tac aag Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 360 365 370	9201
acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 375 380 385	9249
gag ctg aag ggc atc gac ttc aag gag gac ggc aac atc ctg ggg cac Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 390 395 400	9297
aag ctg gag tac aac tac aac agc cac aac gtc tat atc atg gcc gac Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 405 410 415 420	9345
aag cag aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 425 430 435	9393
gag gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 440 445 450	9441
atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 455 460 465	9489

cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc 9537  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 470 475 480

ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag 9585  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu  
 485 490 495 500

ctg tac aag taa agc 9600  
 Leu Tyr Lys

<210> 10

<211> 503

<212> PRT

<213> Artificial sequence

<220>

<223> pVP2-VP3-GFP protein

<400> 10

Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala Val  
 1 5 10 15

Arg Ala Met Glu Ala Ala Ala Asn Val Asp Pro Leu Phe Gln Ser Ala  
 20 25 30

Leu Ser Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp Met  
 35 40 45

Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn Phe  
 50 55 60

Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys Tyr  
 65 70 75 80

Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu Glu  
 85 90 95

Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr Met  
 100 105 110

Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His Arg  
 115 120 125

Gly Pro Ser Pro Gly Gln Val Lys Tyr Trp Gln Asn Lys Arg Glu Ile  
 130 135 140

Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys Ser  
 145 150 155 160

Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile Tyr  
 165 170 175

Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu Val  
 180 185 190

Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu Gln  
 195 200 205



Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn Pro  
 210 215 220  
 Arg Arg Ala Leu Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr Gln  
 225 230 235 240  
 Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp Glu  
 245 250 255  
 Asp Leu Glu Gly Ser Ile Ala Thr Met Val Ser Lys Gly Glu Glu Leu  
 260 265 270  
 Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn  
 275 280 285  
 Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr  
 290 295 300  
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 305 310 315 320  
 Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe  
 325 330 335  
 Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala  
 340 345 350  
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 355 360 365  
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 370 375 380  
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 385 390 395 400  
 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
 405 410 415  
 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
 420 425 430  
 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 435 440 445  
 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 450 455 460  
 Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 465 470 475 480  
 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 485 490 495  
 Gly Met Asp Glu Leu Tyr Lys  
 500